

RAW SEQUENCE LISTING

4

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/524, 750
Source: PCT
Date Processed by STIC: 08/22/2005

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PCT

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DATE: 08/22/2005

PATENT APPLICATION: US/10/524,750

TIME: 17:10:26

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3 <110> APPLICANT: Martin, Gregory B.
 4 Abramovitch, Robert B.
 5 Lin, Nai-Chun
 6 Kim, Young-Jin
 8 <120> TITLE OF INVENTION: BACTERIAL EFFECTOR PROTEINS WHICH INHIBIT PROGRAMMED
 9 CELL DEATH
 11 <130> FILE REFERENCE: 3213/104
 13 <140> CURRENT APPLICATION NUMBER: 10/524,750
 C--> 14 <141> CURRENT FILING DATE: 2005-02-15
 16 <150> PRIOR APPLICATION NUMBER: 60/404,339
 17 <151> PRIOR FILING DATE: 2002-08-16
 19 <150> PRIOR APPLICATION NUMBER: 60/425,842
 20 <151> PRIOR FILING DATE: 2002-11-12
 22 <150> PRIOR APPLICATION NUMBER: PCT/US03/25247
 23 <151> PRIOR FILING DATE: 2003-08-16
 25 <160> NUMBER OF SEQ ID NOS: 54
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1662
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Pseudomonas syringae
 34 <400> SEQUENCE: 1
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 37 caggttcagc cgcgaccctc gaatactccc ccgtcgaacg cgcccgcacc gccgccaacc 180
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 40 gccgcaacgc cgcgtgcaga ggcaagacgc acgcccggagg caactgccga tgcagcgca 360
 41 ccgcgtagag gggcggttgc acacgccaac agtatcgctc agcaattggt cagtgagggc 420
 42 gctgatattt cgcatactcg taacatgctc cgcaatgcaa tgaatggcga cgcagtcgct 480
 43 ttttctcgag tagaacagaa catatttcgc cagcatttcc cgaacatgcc catgcatgga 540
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 46 tcatcatcgg gcagcagtcg gcgttcttta ttggacgggt ttgcccgttt gatggcgcca 720
 47 aaccagggac ggtcgtcgaa cactgccgcc tctcagacgc cggtcgacag gagcccgcga 780
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 51 ttgcagaatg tgggaattaa cccaagtatc gacttggggg aaagccttgt gcaacatccc 1020
 52 ctgctgaatt tgaatgtagc gttgaatcgc atgctggggc tgcgtcccag cgctgaaaga 1080
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 54 cgtgcaacac gattgcggt gatgccggag cgggaggatt acgaaaataa tgtggcttat 1200
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58 ctgggtttta,aggatgcggc agatcatcac acggatgacg tgacgcactg tctttttggc 1440
59 ggagaattgt cgctgagtaa tccggatcag caggtgatcg gtttggcggg taatccgacg 1500
60 gacacgtcgc agccttacag ccaagaggga aataaggacc tggcgttcat ggatatgaaa 1560
61 aaacttgccc aattcctcgc aggcaagcct gagcatccga tgaccagaga aacgcttaac 1620
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74 His Thr Asp Pro Glu Pro Val Ser Gly Gln Ala His Gly Ser Gly Ser
75 20 25 30
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78 35 40 45
80 Thr Pro Pro Ser Asn Ala Pro Ala Pro Pro Pro Thr Gly Arg Glu Arg
81 50 55 60
83 Leu Ser Arg Ser Thr Ala Leu Ser Arg Gln Thr Arg Glu Trp Leu Glu
84 65 70 75 80
86 Gln Gly Met Pro Thr Ala Glu Asp Ala Ser Val Arg Arg Arg Pro Gln
87 85 90 95
89 Val Thr Ala Asp Ala Ala Thr Pro Arg Ala Glu Ala Arg Arg Thr Pro
90 100 105 110
92 Glu Ala Thr Ala Asp Ala Ser Ala Pro Arg Arg Gly Ala Val Ala His
93 115 120 125
95 Ala Asn Ser Ile Val Gln Gln Leu Val Ser Glu Gly Ala Asp Ile Ser
96 130 135 140
98 His Thr Arg Asn Met Leu Arg Asn Ala Met Asn Gly Asp Ala Val Ala
99 145 150 155 160
101 Phe Ser Arg Val Glu Gln Asn Ile Phe Arg Gln His Phe Pro Asn Met
102 165 170 175
104 Pro Met His Gly Ile Ser Arg Asp Ser Glu Leu Ala Ile Glu Leu Arg
105 180 185 190
107 Gly Ala Leu Arg Arg Ala Val His Gln Gln Ala Ala Ser Ala Pro Val
108 195 200 205
110 Arg Ser Pro Thr Pro Thr Pro Ala Ser Pro Ala Ala Ser Ser Ser Gly
111 210 215 220
113 Ser Ser Gln Arg Ser Leu Phe Gly Arg Phe Ala Arg Leu Met Ala Pro
114 225 230 235 240
116 Asn Gln Gly Arg Ser Ser Asn Thr Ala Ala Ser Gln Thr Pro Val Asp
117 245 250 255
119 Arg Ser Pro Pro Arg Val Asn Gln Arg Pro Ile Arg Val Asp Arg Ala
120 260 265 270
122 Ala Met Arg Asn Arg Gly Asn Asp Glu Ala Asp Ala Ala Leu Arg Gly
123 275 280 285
125 Leu Val Gln Gln Gly Val Asn Leu Glu His Leu Arg Thr Ala Leu Glu

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131 Leu Gln Asn Val Gly Ile Asn Pro Ser Ile Asp Leu Gly Glu Ser Leu
132      325      330      335
134 Val Gln His Pro Leu Leu Asn Leu Asn Val Ala Leu Asn Arg Met Leu
135      340      345      350
137 Gly Leu Arg Pro Ser Ala Glu Arg Ala Pro Arg Pro Ala Val Pro Val
138      355      360      365
140 Ala Pro Ala Thr Ala Ser Arg Arg Pro Asp Gly Thr Arg Ala Thr Arg
141      370      375      380
143 Leu Arg Val Met Pro Glu Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr
144 385      390      395      400
146 Gly Val Arg Leu Leu Asn Leu Asn Pro Gly Val Gly Val Arg Gln Ala
147      405      410      415
149 Val Ala Ala Phe Val Thr Asp Arg Ala Glu Arg Pro Ala Val Val Ala
150      420      425      430
152 Asn Ile Arg Ala Ala Leu Asp Pro Ile Ala Ser Gln Phe Ser Gln Leu
153      435      440      445
155 Arg Thr Ile Ser Lys Ala Asp Ala Glu Ser Glu Glu Leu Gly Phe Lys
156      450      455      460
158 Asp Ala Ala Asp His His Thr Asp Asp Val Thr His Cys Leu Phe Gly
159 465      470      475      480
161 Gly Glu Leu Ser Leu Ser Asn Pro Asp Gln Gln Val Ile Gly Leu Ala
162      485      490      495
164 Gly Asn Pro Thr Asp Thr Ser Gln Pro Tyr Ser Gln Glu Gly Asn Lys
165      500      505      510
167 Asp Leu Ala Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly
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178 <211> LENGTH: 1740
179 <212> TYPE: DNA
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185 cgcttgccgg cgctccgga tgcacccgcg tcgcaggcgc gagatcgacg cgaaatgctt 180
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190 ccacacgcca atagaattgt tcaacaattg gttgacgcgg gcgctgatct tgccggtatt 480
191 aacaccatga ttgacaatgc catgcgtcgc cagcgatag ctcttccttc tcgaacagta 540
192 cagagtattt tgatcgagca tttccctcac ctgctagcgg gtgaactcat tagtggctca 600
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196 ggggttgatga cgcctaataca gagacgtccg tcgagcgctt cgaacgcgtc tgccctctcaa 840
197 aggcctgtag acagaagccc gccacgcgta aaccagggtac ccacaggcgc taacagggtt 900
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200 atcccatggg atatagcgta cgccttgagc ggtgtgggca ttgcgccaag tatcgatacg 1080
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202 gggcctcgtc ccgctcgtag tcaagcgccct cgtccagccg ttccgggtggc tcccgcgacc 1200
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208 acgcaatgcc tttttggtga agaattgtcg ctgaccagtt cggatcagca ggtgatcggc 1560
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214 <210> SEQ ID NO: 4

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216 <212> TYPE: PRT

217 <213> ORGANISM: Pseudomonas syringae

219 <400> SEQUENCE: 4

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227             35             40             45
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233             65             70             75             80
235 Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala
236             85             90             95
238 Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp
239             100            105            110
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242             115            120            125
244 Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn
245             130            135            140
247 Arg Ile Val Gln Gln Leu Val Asp Ala Gly Ala Asp Leu Ala Gly Ile
248             145            150            155            160
250 Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro
251             165            170            175
253 Ser Arg Thr Val Gln Ser Ile Leu Ile Glu His Phe Pro His Leu Leu
254             180            185            190
256 Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala
257             195            200            205

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262 Thr Ala Ala Arg Ser Ser Val Arg Thr Pro Glu Arg Ser Thr Val Pro
263 225      230      235      240
265 Pro Thr Ser Thr Glu Ser Ser Ser Gly Ser Asn Gln Arg Thr Leu Leu
266      245      250      255
268 Gly Arg Phe Ala Gly Leu Met Thr Pro Asn Gln Arg Arg Pro Ser Ser
269      260      265      270
271 Ala Ser Asn Ala Ser Ala Ser Gln Arg Pro Val Asp Arg Ser Pro Pro
272      275      280      285
274 Arg Val Asn Gln Val Pro Thr Gly Ala Asn Arg Val Val Met Arg Asn
275      290      295      300
277 His Gly Asn Asn Glu Ala Asp Ala Ala Leu Gln Gly Leu Ala Gln Gln
278 305      310      315      320
280 Gly Val Asp Met Glu Asp Leu Arg Ala Ala Leu Glu Arg His Ile Leu
281      325      330      335
283 His Arg Arg Pro Ile Pro Met Asp Ile Ala Tyr Ala Leu Gln Gly Val
284      340      345      350
286 Gly Ile Ala Pro Ser Ile Asp Thr Gly Glu Ser Leu Met Glu Asn Pro
287      355      360      365
289 Leu Met Asn Leu Ser Val Ala Leu His Arg Ala Leu Gly Pro Arg Pro
290      370      375      380
292 Ala Arg Ala Gln Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr
293 385      390      395      400
295 Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile
296      405      410      415
298 Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu
299      420      425      430
301 Leu Ser Leu Asn Pro Gly Ala Gly Val Arg Glu Thr Val Ala Ala Phe
302      435      440      445
304 Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala
305      450      455      460
307 Ala Leu Asn Leu Ser Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys
308 465      470      475      480
310 Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Ala Ala Asp His
311      485      490      495
313 Pro Asp Asp Ala Thr Gln Cys Leu Phe Gly Glu Glu Leu Ser Leu Thr
314      500      505      510
316 Ser Ser Asp Gln Gln Val Ile Gly Leu Ala Gly Lys Ala Thr Asp Met
317      515      520      525
319 Ser Glu Ser Tyr Ser Arg Glu Ala Asn Lys Asp Leu Val Phe Met Asp
320      530      535      540
322 Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu His Pro Met
323 545      550      555      560
325 Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr Ala Phe Arg
326      565      570      575
328 Ile Val Pro
332 <210> SEQ ID NO: 5
333 <211> LENGTH: 1740

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:352
L:884 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24
L:1253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:1334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
M:341 Repeated in SeqNo=48
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L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
M:341 Repeated in SeqNo=54